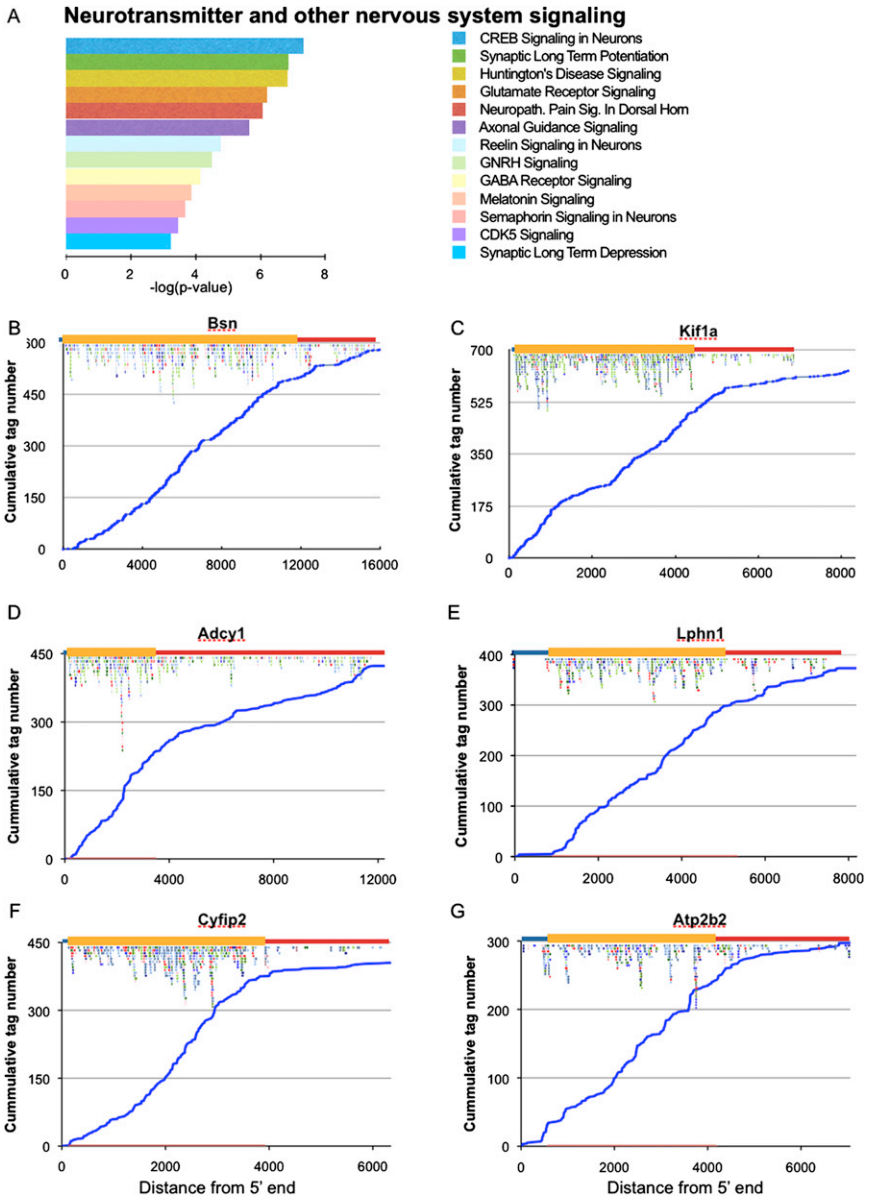

Figure S2. Ingenuity Analysis of FMRP Target Transcripts and Distribution of FMRP CLIP Tags on Individual Transcripts, Related to Figure 2

(A) The top signaling pathways identified by Ingenuity Systems canonical pathway analysis that were enriched for the 842 FMRP target transcripts, plotted as a function of significance (-log(p-value), Fisher's exact test). Pathways with a -log(p-value) > 3 (corresponding to a p-value < 0.001) are shown. FMRP targets found in these pathways are listed in Table S4. We also analyzed Intracellular Signaling and second messenger signaling pathways, and found enrichment in the following pathways (Table S4): Calcium signaling, Protein kinase A signaling, Phospholipase C signaling, G protein coupled receptor signaling, RhoA signaling, Insulin receptor signaling, cAMP-mediated signaling, α-adrenergic signaling and PI3-kinase/Akt signaling.

(B–G) Examples of the distribution of FMRP CLIP tags on individual transcripts are shown as the cumulative tag number as a function of distance in nucleotides from the 5′ end of the mRNA (blue line). Drawings above each figure depict the 5′UTR (blue), coding sequence (gold), and 3′UTR (red). Individual unique tags are shown as colored bars; each color refers to 1 of the 7 separate FMRP CLIP experiments. In general, unique tags are crosslinked with an even distribution along coding sequence, with some tags present in UTRs but at a lower density than in coding sequence. Note, however, that these results do not address FMRP stoichiometry within any individual target mRNA molecule; we currently cannot determine whether FMRP binds once or many times within a single repressed transcript molecule.